

SEQUENCE LISTING

<110> Asundi, Vinod
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Zhou, Hua

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/37665

<150> US 09/687,860

<151> 2000-10-13

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	
cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	
atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	
tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

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tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
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gaa	gac	aca	gaa													300
Glu	Asp	Thr	Glu													
			100													

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Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	
1				5					10					15		

gga	tgt	aag	ttt	ggg	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	96
Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	
			20				25						30			

cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	144
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	
		35					40					45				

atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	192
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	
	50					55					60					

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		

gaa	gac	aca	gaa	gaa	ggg	cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	336
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	
			100					105					110			

cgc	ctg	gcc	cca	aat	gga	aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	384
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	
		115					120					125				

tct	ggg	aaa	gtc	atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	432
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
	130					135					140					

gga	agc	tac	tac	tgc	aaa	tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	480
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	
145					150					155					160	

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agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc	528
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser	
165 170 175	
cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
180 185 190	
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
195 200 205	
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
210 215 220	
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
225 230 235 240	
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
245 250 255	
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
260 265 270	
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
Arg Gly Glu Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
275 280 285	
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
290 295 300	
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
305 310 315 320	
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
325 330 335	
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
340 345 350	
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
355 360 365	
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
370 375 380	
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
385 390 395 400	
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
405 410 415	

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tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa 1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
420 425 430

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
435 440 445

aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
450 455 460

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
485 490 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536
Leu Leu Ser Val Xaa Xaa
500

tatgtcagtt cccctgggtttt tttgatattg catcatagga cctctggcat tttaaaatta 1596
ctagctgaaa aattg 1611

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<213> Homo sapiens

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Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
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Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
50 55 60
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
65 70 75 80
Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
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Glu Asp Thr Glu
100

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Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly
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Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser
	50					55					60				
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr
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Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys
			85						90					95	
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu
			100					105					110		
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala
		115					120					125			
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe
	130					135					140				
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile
145					150					155					160
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser
				165					170					175	
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe
			180				185						190		
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser
	195						200					205			
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr
	210					215					220				
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys
225					230					235					240
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro
				245					250					255	
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser
			260					265					270		
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met
		275					280					285			
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn
	290					295					300				
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val
305					310					315					320
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu
			325						330					335	
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser
			340					345					350		
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe
		355					360					365			
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala
	370					375					380				
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu
385					390					395					400
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp
				405					410					415	
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys
			420					425					430		
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu
		435					440					445			
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr
	450					455					460				
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu
465					470					475					480
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser
				485					490					495	
Leu	Leu	Ser	Val	Asp	Asp	Xaa	Met	Val	Leu	Ser	Leu	Tyr	Leu	Thr	Leu
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Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly
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Ile Leu Lys Leu Leu Ala Glu Lys Leu
530 535

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ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagagg gggctcagga 180
ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231
Met Pro Leu Pro Trp Ser Leu Ala Leu
1 5

ccg ctg ctg ctc ccc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279
Pro Leu Leu Leu Pro Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
10 15 20 25

gca agg cat cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt 327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys
30 35 40
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc 375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser
45 50 55

aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag 423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu
60 65 70

tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa 471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys
75 80 85

acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc 519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys
90 95 100 105

caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc 567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu
110 115 120

agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca 615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr
125 130 135

tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg 663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly
140 145 150

cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga 711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly
155 160 165

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aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	

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			20					25					30			
Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala	
		35					40					45				

Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
50						55					60				
Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
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Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
				85					90					95	
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
			100					105					110		
His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
		115					120					125			
Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
		130					135				140				
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145					150					155					160
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
				165					170					175	
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
			180					185					190		
Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
		195					200					205			
Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr
		210				215					220				
Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln
225					230					235					240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
				245					250					255	
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
			260					265					270		
Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
		275					280					285			
Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
		290				295					300				
Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
305					310					315					320
Ile	Val	Ser	Arg	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	
				325				330						335	
Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
			340					345					350		
Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
		355					360					365			
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
		370				375					380				
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
385					390					395					400
Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu
				405					410					415	
Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe
			420					425					430		
Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	Arg
		435					440					445			
Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu
		450				455					460				
Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val
465					470					475					480
Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser
				485					490					495	
Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr
			500					505					510		
Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys
		515					520					525			
Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys
		530				535					540				

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Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 7
<211> 42
<212> PRT
<213> Drosophila Melanogaster

<220>
<221> VARIANT
<222> (1)...(42)
<223> Xaa = Any Amino Acid

<400> 7
Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
1 5 10 15
Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
20 25 30
Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
35 40

<210> 8
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(39)
<223> Xaa = Any Amino Acid

<400> 8
Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
1 5 10 15
Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
20 25 30
Gly Xaa Xaa Leu Xaa Cys Asp
35

<210> 9
<211> 164
<212> PRT
<213> Homo sapiens

<400> 9
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn
1 5 10 15
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
20 25 30
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
35 40 45
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
50 55 60
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
65 70 75 80
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
85 90 95
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
100 105 110
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
115 120 125
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
130 135 140

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Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
 145 150 155 160
 Leu Arg Cys Ser

<210> 10
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(45)
 <223> Xaa = Any Amino Acid

<400> 10
 Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa
 1 5 10 15
 Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly
 20 25 30
 Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp
 35 40 45

<210> 11
 <211> 58
 <212> PRT
 <213> Mammalian

<220>
 <221> VARIANT
 <222> (1)...(58)
 <223> Xaa = Any Amino Acid

<400> 11
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 1 5 10 15
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 20 25 30
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
 35 40 45
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
 50 55

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-52

<400> 12
 ctcacacctca agccctctt t

21

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene-specific PCR primer 10244-51

<400> 13

105401 549550

ccatgagagt tccccgctct g 21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer T7

<400> 14
gtaatacgac tcactatagg g 21

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector primer SP6

<400> 15
atttagtgga cactatagaa gg 22

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-A

<400> 16
cccaggctga cgtgccgatg c 21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene-specific PCR primer 10244-B

<400> 17
gcagcaggcc agttagttc c 21

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(502)
<223> Xaa = Any Amino Acid

<400> 18
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
1 5 10 15
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

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Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	50	55	60
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	65	70	75
Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	85	90	95
Glu	Asp	Thr	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu		100	105	110
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	115	120	125
Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	130	135	140
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	145	150	155
Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	165	170	175
His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	180	185	190
Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	195	200	205
Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	210	215	220
Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	225	230	235
Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	245	250	255
Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	260	265	270
Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	275	280	285
Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	290	295	300
Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	305	310	315
Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	325	330	335
Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	340	345	350
Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	355	360	365
Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	370	375	380
Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	385	390	395
Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	405	410	415
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	420	425	430
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	435	440	445
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr	450	455	460
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu	465	470	475
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser	485	490	495
Leu	Leu	Ser	Val	Xaa	Xaa											500		

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 19
 gtcatttctg aatctttcca c 21
 <210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 20
 gaaatgttgc agagagaagc tc 22
 <210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 21
 ccagaaccca ccaggactcc 20
 <210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 22
 gggaactgac atacaaagtc
 <210> 23
 <211> 2365
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (205)..(1863)
 <400> 23
 actagtgatt ccacctaata acgactcact atagggctcg agcggccgcc cgggcaggtc 60
 tgcagggaca gcacccggta actgcgagtg gagcggagga cccgagcggc tgaggagaga 120
 ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagagg gggctcagga 180
 ggaggaagga ggaccctgac gaga atg cct ctg ccc tgg agc ctt gcg ctc 231
 Met Pro Leu Pro Trp Ser Leu Ala Leu
 1 5
 ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279
 Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
 10 15 20 25

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gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt	327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys	
30 35 40	
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc	375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser	
45 50 55	
aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	

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aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser	
350 355 360	
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc	1335
Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	
ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac	1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp	
460 465 470	
aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg	1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu	
475 480 485	
gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa	1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys	
490 495 500 505	
att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa	1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu	
510 515 520	
gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc	1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val	
525 530 535	

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ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
540 545 550

tgaatgttac tatctttata ttgactttg tatgtcagtt ccttggtttt ttgatattg 1923
satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983
aaattattat tgtaagatgc ctttmttgta taagatatgc caatatttgc tttaaatattc 2043
atatcactgt atctttctcag tcattttctga atctttccac attatattat aaaatatgga 2103
aatgtcaggt ttatctcccc tcttcagtat atctgatttg tataagtaag ttgatgagct 2163
tctctctgca acattttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223
actcttatga tagtttttgg aaactatgac atcaaagata gacttttgcc taagtggctt 2283
agctgggtct ttcatatgcca aacttgtata tttaaattct ttgtaataat aatatccaaa 2343
tcatcaaaaa aaaaaaaaaa aa 2365

<210> 24
<211> 553
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(553)

<400> 24

Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu Ser Trp Val
1 5 10 15
Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly Leu Leu
20 25 30
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
50 55 60
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
65 70 75 80
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
85 90 95
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
100 105 110
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
115 120 125
Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
130 135 140
Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
145 150 155 160

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Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
165 170 175

Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn
275 280 285

Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
355 360 365

Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val
385 390 395 400

Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu
405 410 415

Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe
420 425 430

Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg
435 440 445

Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu
450 455 460

Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val
465 470 475 480

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser
485 490 495

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Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr
500 505 510

Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys
515 520 525

Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys
530 535 540

Pro Asp Ser Leu Leu Ser Val Asp Asp
545 550

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ccctggcatg ggagaagacc ac 22

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gtgatatgat atttaaagca aatattggca 30

<210> 27
<211> 2360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (190)..(1869)

<220>
<221> misc_feature
<222> (1)...(2360)
<223> n = a,t,c or g

<400> 27
cctctatatg catgctcgag cgcggnccgca gtgtgatgga tatctgcaga attcggctta 60

ctcactatag ggctcgagcg gccgcccggg caggtgagga gagaggaggc ggccggcttag 120

ctgctacggg gtccggggccg gcgcctccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
1 5 10

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tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct	276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser	
14 19 24 29	
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His His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly	
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Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg	
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aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt	420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe	
62 67 72 77	
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Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr	
78 83 88 93	
ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg	516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg	
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Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe	
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Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser	
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Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu	
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Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro	
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Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val	
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Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr	
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Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr	
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cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc	948
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Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu	
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Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg	
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Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys	
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att aaa aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg	1140
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Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn	
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Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu	
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Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly	
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Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu	
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Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu	
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Ala Gly His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp	
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Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala	
462 467 472 477	
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Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn	
478 483 488 493	
gcc ctg gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca	1716
Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr	
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 Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile
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 ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat 1812
 Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp
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 ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg 1860
 Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val
 542 547 552 557
 gat gac tga atgttac tatctttata tttgactttg tatgtcagtt ccctggtttt 1916
 Asp Asp *
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 taccaacaga aatattattg taagatgcct ttcttgtata agatatgcca atatttgctt 2036
 taaatatcat atcactgtat cttctcagtc atttctgaat ctttccacat tatattataa 2096
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 Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys
 50 55 60
 Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys
 65 70 75 80
 Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr
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 Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln
 100 105 110
 His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser
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Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	145	150	155
Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	165	170	175
Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	180	185	190
Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	195	200	205
His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	210	215	220
Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	225	230	235
Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	245	250	255
Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	260	265	270
Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	275	280	285
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Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	325	330	335
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	340	345	350
Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	355	360	365
Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	370	375	380
Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	385	390	395
Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	405	410	415
Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	420	425	430
Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	435	440	445
Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	450	455	460

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 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
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 Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His
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 His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly
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 Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val
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 Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly
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Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser	
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Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg	
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tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc cac	564
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His	
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Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met	
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Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys	
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158 163 168 173	
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Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile	
190 195 200 205	
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Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile	
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Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu	
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Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu	
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gct cac aaa aac agt atg aaa aag aag gca aaa att aaa aat gtt acc	1092
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cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc ttc	1140
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Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys	
318 323 328 333	

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	50					55					60				
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Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val
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Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn
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Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met
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 275 280 285

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Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn
 325 330 335

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Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe
 355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln
 370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser
 385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg
 405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly
 420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
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Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
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Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
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Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr
 485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
 500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
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Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg
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cat cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat      386
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr
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gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga      434
Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly
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gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg      482
Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val
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gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc      530
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys
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agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac      578
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His
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aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc      626
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly
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cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc      674
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala
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atg ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag      722
Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln
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tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac      770
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp
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Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr	
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aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac	866
Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His	
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Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp	
205 210 215	
ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat	962
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn	
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Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr	
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aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct gtg aag	1058
Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys	
255 260 265	
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Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu	
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Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val	
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Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro	
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly	
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Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys	
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Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His
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Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro
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Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys
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Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
35 40 45

Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
50 55 60

Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
65 70 75 80

Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
85 90 95

Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
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Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln
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Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser
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Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp
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Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val
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Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu
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Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr
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Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu
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Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala
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Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr
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Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu
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Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala
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Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe
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 Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg
 370 375 380
 Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala Asp Leu Asn Ile Ser
 385 390 395 400
 Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg
 405 410 415
 Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly
 420 425 430
 Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly
 435 440 445
 Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys
 450 455 460
 Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg
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 Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly
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 Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly
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 Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
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